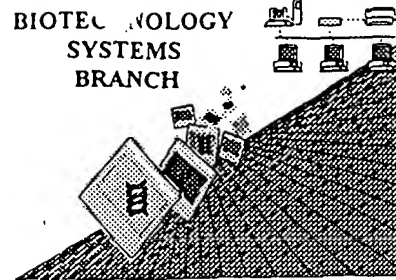# RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _O9/785, 738_

Source: _OiPE_

Date Processed by STIC: _6-6-01_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: *09/785,738*

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
       Wrapped Aminos·   was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
       prevent "wrapping."

2____Invalid Line Length   The rules require that a line not exceed 72 characters in length. This includes white spaces.

3____Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
       Numbering   use space characters, instead.

4____Non-ASCII   The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
       ensure your subsequent submission is saved in ASCII text.

5____Variable Length   Sequence(s)___contain n's or Xaa's representing more than one residue. Per Sequence Rules,
       each n or Xaa can only represent a single residue. Please present the maximum number of each
       residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
       "bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
       previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
       the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
       Artificial or Unknown sequences.

7____Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
       (OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
       (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
       (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
       This sequence is intentionally skipped

       Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8____Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
       (NEW RULES)   <210> sequence id number
       <400> sequence id number
       000

9 ✓ Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
       (NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
       In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10____Invalid <213>   Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
       Response   scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
       is Artificial Sequence

11____Use of <220>   Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
       Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
       "Unknown." Please explain source of genetic material in <220> to <223> section.
       (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12____PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
       "bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
       listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING   DATE: 05/31/2001
PATENT APPLICATION: US/09/785,738   TIME: 10:36:54

Input Set : **A:\es.txt**
Output Set: **C:\CRF3\05312001\I785738.raw**

```
   3 <110> APPLICANT: Sauter, Margret M.
   4        Lorbiecke, Rene
   6 <120> TITLE OF INVENTION: ALTERATION OF GROWTH AND ADAPTATION UNDER HYPOXIC
   7        CONDITIONS
   9 <130> FILE REFERENCE: CropDesign
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/785,738
C--> 12 <141> CURRENT FILING DATE: 2001-02-16
  14 <160> NUMBER OF SEQ ID NOS: 18
  16 <170> SOFTWARE: PatentIn Ver. 2.1
```

Does Not Comply
Corrected Diskette Needed

pp. 1-11

ERRORED SEQUENCES

```
  18 <210> SEQ ID NO: 1
  19 <211> LENGTH: 872
  20 <212> TYPE: DNA
  21 <213> ORGANISM: Rice
  23 <220> FEATURE:
  24 <221> NAME/KEY: CDS
  25 <222> LOCATION: (69)..(668)
  27 <400> SEQUENCE: 1
  28 agacgaacaa aaaacagaat ccatcgccat aatcgaaggt tcgctcttgc ttccaccccg 60
  29 caatccac atg gag aac gaa ttc cag gat ggt aag acg gag gtg ata gaa 110
  30         Met Glu Asn Glu Phe Gln Asp Gly Lys Thr Glu Val Ile Glu
W--> 31           1               5                  10
W--> 33 gca tgg tac atg gat gat agc gaa gag gac cag agg ctt cct cat cac 158 Ala Trp
W--> 34 Tyr Met Asp Asp Ser Glu Glu Asp Gln Arg Leu Pro His His
W--> 35  15              20                 25              30
W--> 37 cgc gaa ccc aaa gaa ttc att cct gtt gat aag ctt aca gaa cta gga 206 Arg Glu
W--> 38 Pro Lys Glu Phe Ile Pro Val Asp Lys Leu Thr Glu Leu Gly
W--> 39          35                 40                 45
W--> 41 gta atc agc tgg cgc cta aat cct gat aac tgg gag aat tgc gag aac 254 Val Ile
W--> 42 Ser Trp Arg Leu Asn Pro Asp Asn Trp Glu Asn Cys Glu Asn
W--> 43          50                 55                 60
W--> 45 ctg aag aga atc cgc gaa gcc aga ggt tac tct tat gtg gac att tgt 302 Leu Lys
W--> 46 Arg Ile Arg Glu Ala Arg Gly Tyr Ser Tyr Val Asp Ile Cys
W--> 47          65                 70                 75
W--> 49 gat gtg tgc cca gag aag ctg cca aat tat gaa act aag atc aag agt 350 Asp Val
W--> 50 Cys Pro Glu Lys Leu Pro Asn Tyr Glu Thr Lys Ile Lys Ser
W--> 51          80                 85                 90
W--> 53 ttc ttt gaa gaa cac ctg cat acc gat gaa gaa ata cgc tat tgt ctt 398 Phe Phe
W--> 54 Glu Glu His Leu His Thr Asp Glu Glu Ile Arg Tyr Cys Leu
W--> 55          95                 100                105             110
W--> 57 gaa ggg agt gga tac ttt gat gtg aga gac caa aat gat cag tgg att 446 Glu Gly
N--> 58 Ser Gly Tyr Phe Asp Val Arg Asp Gln Asn Asp Gln Trp Ile
N--> 59          115                120                125
N--> 61 cgt ata gca ctg aag aaa gga ggc atg att gtt ctg cct gca ggg atg 494 Arg Ile
```

move to here

Format errors. move underlined amino acids to the end of the line. Then insert "hard return" where arrows indicate.

RAW SEQUENCE LISTING   DATE: 05/31/2001
PATENT APPLICATION: US/09/785,738   TIME: 10:36:54

Input Set : A:\es.txt
Output Set: C:\CRF3\05312001\I785738.raw

```
W--> 62 Ala Leu Lys Lys Gly Gly Met Ile Val Leu Pro Ala Gly Met
W--> 63             130                 135                 140
W--> 65 tac cac cgc ttt acg ttg gac acc gac aac tat atc aag gca atg cga   542 Tyr His
W--> 66 Arg Phe Thr Leu Asp Thr Asp Asn Tyr Ile Lys Ala Met Arg
W--> 67             145                 150                 155
W--> 69 ctg ttt gtt ggc gat cct gtt tgg aca ccc tac aac cgt ccc cat gac   590 Leu Phe
W--> 70 Val Gly Asp Pro Val Trp Thr Pro Tyr Asn Arg Pro His Asp
W--> 71             160                 165                 170
W--> 73 cat ctt cct gca aga aag gag ttt ttg gct aaa ctt ctc aag tca gaa   638 His Leu
W--> 74 Pro Ala Arg Lys Glu Phe Leu Ala Lys Leu Leu Lys Ser Glu
W--> 75 175                 180                 185                 190
W--> 77 ggt gaa aat caa gca gtt gaa ggc ttc tga gggttttgtt gggctcctgc   688 Gly Glu
W--> 78 Asn Gln Ala Val Glu Gly Phe
W--> 79             195                 200
E--> 81 actgcggttc tatattcaac ctgaataaga tgtgctatag caatgtaaat ttagcacagt 748
E--> 82 ggctatggtc gccactcacc aacttgaagt gaaagattta atgattttg ttaattctta 808
E--> 83 tgtatcaatc ggcatatagc atttccgaaa tgtgttttca ataaacagga gtcatgaagc 868
E--> 84 tgaa                                                            872
    121 <210> SEQ ID NO: 3
    122 <211> LENGTH: 980
    123 <212> TYPE: DNA
    124 <213> ORGANISM: Rice
    126 <220> FEATURE:
    127 <221> NAME/KEY: CDS
    128 <222> LOCATION: (139)..(735)
    130 <400> SEQUENCE: 3
    131 cggacgcgtg ggcagattgc gttgagctga agctgttcgt gtgactcttc tacaccttcc 60
    132 aggctatccg gaatcgggag ggtttcccaa taggaaagca actcaggact caggagcggc 120
    133 gtctgagagg tttcagag atg gag aac cag ttc cag gat ggc aag gag gag   171
    134                    Met Glu Asn Gln Phe Gln Asp Gly Lys Glu Glu
W--> 135                    1                 5                   10
W--> 137 gtc atc gaa gct tgg tac atg gat gac agt gaa gag gac cag agg ctt   219 Val Ile
W--> 138 Glu Ala Trp Tyr Met Asp Asp Ser Glu Glu Asp Gln Arg Leu
    139             15                  20                  25
W--> 141 cct cat cat cgt gag ccc aaa gaa ttc att cct ctt agc aaa ctt tca   267 Pro His
W--> 142 His Arg Glu Pro Lys Glu Phe Ile Pro Leu Ser Lys Leu Ser
W--> 143             30                  35                  40
W--> 145 gag tta gga ata tta agc tgg cgc ctg aat gct gat gac tgg gag aat   315 Glu Leu
W--> 146 Gly Ile Leu Ser Trp Arg Leu Asn Ala Asp Asp Trp Glu Asn
W--> 147             45                  50                  55
W--> 149 gat gag aac ctc aag aaa atc cgt gag gcc agg gga tac tct tac atg   363 Asp Glu
W--> 150 Asn Leu Lys Lys Ile Arg Glu Ala Arg Gly Tyr Ser Tyr Met
W--> 151 60                  65                  70                  75
W--> 153 gat att tgt gat gtg tgt cca gaa aag ctg cca aac tat gag gct aag   411 Asp Ile
W--> 154 Cys Asp Val Cys Pro Glu Lys Leu Pro Asn Tyr Glu Ala Lys
W--> 155             80                  85                  90
W--> 157 ctg aaa aat ttc ttt gaa gaa cac ttg cat act gat gaa gag ata cgc   459 Leu Lys
W--> 158 Asn Phe Phe Glu Glu His Leu His Thr Asp Glu Glu Ile Arg
W--> 159             95                  100                 105
```

RAW SEQUENCE LISTING   DATE: 05/31/2001
PATENT APPLICATION: US/09/785,738   TIME: 10:36:54

Input Set : A:\es.txt
Output Set: C:\CRF3\05312001\I785738.raw

Same

```
W--> 161  tat tgt ctt gag gga agt gga tac ttc gat gtc agg gac caa aat gat   507 Tyr Cys
W--> 162  Leu Glu Gly Ser Gly Tyr Phe Asp Val Arg Asp Gln Asn Asp
W--> 163            110               115                   120
W--> 165  cag tgg atc cgt gta gca gtg aag aaa ggg ggc atg att gtt ttg cct   555 Gln Trp
W--> 166  Ile Arg Val Ala Val Lys Lys Gly Gly Met Ile Val Leu Pro
W--> 167            125               130                   135
W--> 169  gcg gga atg tat cac cgc ttc aca ttg gac agt gac aac tac atc aag   603 Ala Gly
W--> 170  Met Tyr His Arg Phe Thr Leu Asp Ser Asp Asn Tyr Ile Lys
W--> 171  140               145               150                   155
W--> 173  gca atg cgg ctc ttt gtg gga gag cct gtc tgg acg ccg tac aac cgt   651 Ala Met
W--> 174  Arg Leu Phe Val Gly Glu Pro Val Trp Thr Pro Tyr Asn Arg
W--> 175            160               165                   170
W--> 177  ccc cat gac cat ctg cca gct aga aag gag tat gtc gaa aaa att atc   699 Pro His
W--> 178  Asp His Leu Pro Ala Arg Lys Glu Tyr Val Glu Lys Ile Ile
W--> 179            175               180                   185
W--> 181  aac agg ggt gga act caa gct gtc gaa gct cgt taa aggcatatca        745 Asn Arg
W--> 182  Gly Gly Thr Gln Ala Val Glu Ala Arg
W--> 183            190               195
E--> 185  agatgtgctt cctagttcgg tgttctgtta cactctacag atactgaata aactgtgcta 805
E--> 186  tcagctgttg caatgggctc ctaccgacat cttacatcat ttggcagtat tttgcacaaa 865
E--> 187  cccgcttaaa atctccctga aaatacgcac gtcaccatgt cagagtgttt atatacaata 925
E--> 188  atgacacttc agtccacagt cagcaaggga ctaatgacaa aaaaaaaaaa aaaaa       980
      225  <210> SEQ ID NO: 5
      226  <211> LENGTH: 774
      227  <212> TYPE: DNA
      228  <213> ORGANISM: Tomato
      230  <220> FEATURE:
      231  <221> NAME/KEY: CDS
      232  <222> LOCATION: (1)..(591)
      234  <400> SEQUENCE: 5
```

Same

```
W--> 235  gca cca gat cca aga gag gat gtc ata cag gca tgg tac atg gat gac    48 Ala Pro Asp
W--> 236  Pro Arg Glu Asp Val Ile Gln Ala Trp Tyr Met Asp Asp
W--> 237  1                 5                 10                  15
W--> 239  aac gat gag gac cag agg ctt cct cat cac cgt gag cca aag gaa ttt    96 Asn Asp Glu
W--> 240  Asp Gln Arg Leu Pro His His Arg Glu Pro Lys Glu Phe
W--> 241            20                25                  30
W--> 243  gtg tct ctt gac aag ctg gct gaa ctt gga gtg ctc agc tgg aga ctt   144 Val Ser
W--> 244  Leu Asp Lys Leu Ala Glu Leu Gly Val Leu Ser Trp Arg Leu
W--> 245            35                40                  45
W--> 247  gat gct gac aat tat gag act gat gag gag ttg aag aaa att cgg gaa   192 Asp Ala
W--> 248  Asp Asn Tyr Glu Thr Asp Glu Glu Leu Lys Lys Ile Arg Glu
W--> 249            50                55                  60
W--> 251  gat cgt gga tat tca tac att gat ttc tgt gag gtt tgc cct gag aaa   240 Asp Arg
W--> 252  Gly Tyr Ser Tyr Ile Asp Phe Cys Glu Val Cys Pro Glu Lys
W--> 253  65                70                75                  80
W--> 255  cta ccg aat tac gag gag aaa atc aag aac ttt ttt gaa gaa cac ctg   288 Leu Pro
W--> 256  Asn Tyr Glu Glu Lys Ile Lys Asn Phe Phe Glu Glu His Leu
W--> 257            85                90                  95
W--> 259  cac acc gac gag gag atc cgt tac gct gtt gca gga agt ggt tac ttt   336 His Thr
```

RAW SEQUENCE LISTING   DATE: 05/31/2001
PATENT APPLICATION: US/09/785,738   TIME: 10:36:54

Input Set : A:\es.txt
Output Set: C:\CRF3\05312001\I785738.raw

```
W--> 260 Asp Glu Glu Ile Arg Tyr Ala Val Ala Gly Ser Gly Tyr Phe
W--> 261          100                 105                 110
W--> 263 gat gtc cgc gat gtg aat gag agc tgg att cgc gtc tgg gta aag aaa   384 Asp Val
W--> 264 Arg Asp Val Asn Glu Ser Trp Ile Arg Val Trp Val Lys Lys
W--> 265          115                 120                 125
W--> 267 ggt gga atg att gtt ctt cct gct gga atc tat cac cgc ttc acg ctt   432 Gly Gly
W--> 268 Met Ile Val Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu
W--> 269          130                 135                 140
W--> 271 gat tca agc aac tac att aag gca atg cgt ctc ttt gtt ggt gac cca   480 Asp Ser
W--> 272 Ser Asn Tyr Ile Lys Ala Met Arg Leu Phe Val Gly Asp Pro
W--> 273 145                 150                 155                 160
W--> 275 att tgg act cca tac aat cgt cca cat gat cat ctt ccc gca agg caa   528 Ile Trp
W--> 276 Thr Pro Tyr Asn Arg Pro His Asp His Leu Pro Ala Arg Gln
W--> 277                 165                 170                 175
W--> 279 gaa tat gtt gag acg ttt gtc aac gca gat ggc gct ggt cgt gct gtt   576 Glu Tyr
W--> 280 Val Glu Thr Phe Val Asn Ala Asp Gly Ala Gly Arg Ala Val
W--> 281                 180                 185                 190
W--> 283 aat gct gct gct taa atcaactata ggagaggaat ttgaaatcgt actagattgt   631 Asn Ala
W--> 284 Ala Ala
W--> 285          195
E--> 287 aataaatatt accatatggt ggctttgctg ttcttgatgt gtgccttact aagcatgttt 691
E--> 288 aatgttgtat tgtggcacta aataaatcac cccctatggg agattgattg tttatatgca 751
E--> 289 agtggaattt attatgtgat ttt                                         774
     327 <210> SEQ ID NO: 7
     328 <211> LENGTH: 603
     329 <212> TYPE: DNA
     330 <213> ORGANISM: Tomato
     332 <220> FEATURE:
     333 <221> NAME/KEY: CDS
     334 <222> LOCATION: (3)..(572)
     336 <400> SEQUENCE: 7
W--> 337 aa atg gca atc gag tgt aag gca tgg ttt atg gat gaa aat tca gaa   47     Met Ala
W--> 338 Ile Glu Cys Lys Ala Trp Phe Met Asp Glu Asn Ser Glu
W--> 339    1                 5                 10                 15
W--> 341 gat cag cgg cta ccg cac cag aag aac cca ccg gag ttt gtt tca gtg   95 Asp Gln Arg
W--> 342 Leu Pro His Gln Lys Asn Pro Pro Glu Phe Val Ser Val
W--> 343                 20                 25                 30
W--> 345 gag aaa tta gca gta atc gga gtt tta tac tgg aaa ttg aac cct aat   143 Glu Lys
W--> 346 Leu Ala Val Ile Gly Val Leu Tyr Trp Lys Leu Asn Pro Asn
W--> 347              35                 40                 45
W--> 349 gat tac gag aac gat gaa gaa ttg aaa aaa att cgt caa agt aga ggc   191 Asp Tyr
W--> 350 Glu Asn Asp Glu Glu Leu Lys Lys Ile Arg Gln Ser Arg Gly
W--> 351          50                 55                 60
W--> 353 tac agc tac atg gac ttg ctg gat ttg tgc cct gag aag gtg gat aac   239 Tyr Ser
W--> 354 Tyr Met Asp Leu Leu Asp Leu Cys Pro Glu Lys Val Asp Asn
W--> 355          65                 70                 75
W--> 357 tat gag cag aag ttg aaa aat ttc tat acg gag cac ata cac gca gat   287 Tyr Glu
W--> 358 Gln Lys Leu Lys Asn Phe Tyr Thr Glu His Ile His Ala Asp
W--> 359 80                 85                 90                 95
```

```
RAW SEQUENCE LISTING                     DATE: 05/31/2001
PATENT APPLICATION:  US/09/785,738       TIME: 10:36:54

Input Set : A:\es.txt
Output Set: C:\CRF3\05312001\I785738.raw
```

```
W--> 361 gag gag ata cgt tac tgt ctg gaa ggg agt gga tat ttt gat gtg aga   335 Glu Glu
W--> 362 Ile Arg Tyr Cys Leu Glu Gly Ser Gly Tyr Phe Asp Val Arg
W--> 363              100              105              110
W--> 365 gac aag gat gat cgc tgg att cgc atc tgg atg aag gcc ggt gat atg   383 Asp Lys
W--> 366 Asp Asp Arg Trp Ile Arg Ile Trp Met Lys Ala Gly Asp Met
W--> 367              115              120              125
W--> 369 att gtc ttg cct gct ggg att tac cac cgg ttc acc cta gat act gat   431 Ile Val
W--> 370 Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu Asp Thr Asp
W--> 371              130              135              140
W--> 372 aac tat gtc aag ttg atg agg ttg ttt gtg gga gag ccg gtg tgg acg   479 Asn Tyr
W--> 373 Val Lys Leu Met Arg Leu Phe Val Gly Glu Pro Val Trp Thr
W--> 374              145              150              155
W--> 376 cct tac aat cga cca caa gaa gat cat cca gca agg aag gag tac atc   527 Pro Tyr
W--> 377 Asn Arg Pro Gln Glu Asp His Pro Ala Arg Lys Glu Tyr Ile
W--> 378 160              165              170              175
W--> 380 aag agt gtt act gaa aga gta gga gtg cct ctt aca gca cac taa   572 Lys Ser
W--> 381 Val Thr Glu Arg Val Gly Val Pro Leu Thr Ala His
W--> 382              180              185              190
E--> 384 gacatatttg agctttacaa acctgagagt g                            603
    420 <210> SEQ ID NO: 9
    421 <211> LENGTH: 889
    422 <212> TYPE: DNA
    423 <213> ORGANISM: Soybean
    425 <220> FEATURE:
    426 <221> NAME/KEY: CDS
    427 <222> LOCATION: (32)..(634)
    429 <400> SEQUENCE: 9
    430 cgaacccgtc gtagcagaaa aacttgtcac c atg gtt tct tcc gac aag gat   52
    431 Met Val Ser Ser Asp Lys Asp
W--> 432                                        1                5
W--> 434 cca cga gag gat gtc ctt caa gcc tgg tac atg gat gat agt gat gaa   100 Pro Arg
W--> 435 Glu Asp Val Leu Gln Ala Trp Tyr Met Asp Asp Ser Asp Glu
    436              10              15              20
W--> 438 gat caa aga ctc ccc cac cac aaa gaa ccc aag gag ttt gtc tcg ttg   148 Asp Gln
W--> 439 Arg Leu Pro His His Lys Glu Pro Lys Glu Phe Val Ser Leu
W--> 440 25              30              35
W--> 442 gac caa ctt gct gaa ctt gga gtc ctt agc tgg aaa cta gat gct gat   196 Asp Gln
N--> 443 Leu Ala Glu Leu Gly Val Leu Ser Trp Lys Leu Asp Ala Asp
N--> 444 40              45              50              55
N--> 446 aac cat gaa aat gat cca gag ctg aag aag att cgt gaa gag cgt ggt   244 Asn His
N--> 447 Glu Asn Asp Pro Glu Leu Lys Lys Ile Arg Glu Glu Arg Gly
N--> 448              60              65              70
N--> 450 tac acc tac atg gat gtt tgt gag gtc tgc cca gaa aag ttg cca aat   292 Tyr Thr
N--> 451 Tyr Met Asp Val Cys Glu Val Cys Pro Glu Lys Leu Pro Asn
N--> 452              75              80              85
N--> 454 tat gaa cag aaa atc aaa agc ttc ttt gaa gag cat ctt cac act gat   340 Tyr Glu
N--> 455 Gln Lys Ile Lys Ser Phe Phe Glu Glu His Leu His Thr Asp
N--> 456              90              95              100
N--> 458 gag gag atc cgc ttt tgt gct gct gga agt ggc tat ttt gat gtt agg   388 Glu Glu
```

RAW SEQUENCE LISTING   DATE: 05/31/2001
PATENT APPLICATION: US/09/785,738   TIME: 10:36:54

Input Set : **A:\es.txt**
Output Set: **C:\CRF3\05312001\I785738.raw**

```
W--> 459 Ile Arg Phe Cys Ala Ala Gly Ser Gly Tyr Phe Asp Val Arg
W--> 460      105              110               115
W--> 462 gat cgc aat gaa gct tgg att cgt gtg tgg gtc aag aaa gga gga atg   436 Asp Arg
W--> 463 Asn Glu Ala Trp Ile Arg Val Trp Val Lys Lys Gly Gly Met
W--> 464 120              125              130               135
W--> 466 atc atc tta cct gcc gga att tat cat cgc ttt acg cta gat gag agc   484 Ile Ile
W--> 467 Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu Asp Glu Ser
W--> 468              140              145               150
W--> 470 aac tac att aag gct ttg cgt ttt ttt gtt ggt gag cca gtt tgg act   532 Asn Tyr
W--> 471 Ile Lys Ala Leu Arg Phe Phe Val Gly Glu Pro Val Trp Thr
W--> 472              155              .160              165
W--> 474 cca tac aat cgt cca aat gac cat ctc cct gca aga caa caa tat gtc   580 Pro Tyr
W--> 475 Asn Arg Pro Asn Asp His Leu Pro Ala Arg Gln Gln Tyr Val
W--> 476              170              175               180
W--> 478 aag gat ttt gtg gaa aag gat gtt agc agc cat gct gtt gat gcc acc   628 Lys Asp
W--> 479 Phe Val Glu Lys Asp Val Ser Ser His Ala Val Asp Ala Thr
W--> 480              185              190               195
W--> 482 gcg taa gatctggttc tgcctaatca tagtaccaca tgaaaaggac caagactttg   684 Ala
W--> 483 200
E--> 485 ttgctaaagt aaggtttgaa aaaaagaaaa taatggtgtc tttaaataaa gggtcctggc 744
E--> 486 ttgttatgcc ttgatgtacc ctcgccagtg tttttgttgc ctgtccctgt ataaagattg 804
E-->' 487 cattgtatta ttattagaat tgggtacaga ataaacataa gcataagtta gcatgctgat 864
E--> 488 gtatatttat gtaaaaaaaa ataaa                                       889
     492 <210> SEQ ID NO: 10
     493 <211> LENGTH 200
     494 <212> TYPE: PRT
     495 <213> ORGANISM: Soybean
     497 <400> SEQUENCE: 10
     498 Glu Pro Val Val Ala Glu Lys Leu Val Thr Met Val Ser Ser Asp Lys
     499 1              5               10                15
     500 Asp Pro Arg Glu Asp Val Leu Gln Ala Trp Tyr Met Asp Asp Ser Asp
     501              20              25                30
     502 Glu Asp Gln Arg Leu Pro His His Lys Glu Pro Lys Glu Phe Val Ser
     503              35              40                45
     504 Leu Asp Gln Leu Ala Glu Leu Gly Val Leu Ser Trp Lys Leu Asp Ala
     505      50              55               60
     506 Asp Asn His Glu Asn Asp Pro Glu Leu Lys Lys Ile Arg Glu Glu Arg
     507 65              70               75                80
     508 Gly Tyr Thr Tyr Met Asp Val Cys Glu Val Cys Pro Glu Lys Leu Pro
     509              85              90                95
     510 Asn Tyr Glu Gln Lys Ile Lys Ser Phe Phe Glu Glu His Leu His Thr
     511              100             105               110
     512 Asp Glu Glu Ile Arg Phe Cys Ala Ala Gly Ser Gly Tyr Phe Asp Val
     513              115             120               125
     514 Arg Asp Arg Asn Glu Ala Trp Ile Arg Val Trp Val Lys Lys Gly Gly
     515      130             135              140
     516 Met Ile Ile Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu Asp Glu
     517 145              150             155               160
     518 Ser Asn Tyr Ile Lys Ala Leu Arg Phe Phe Val Gly Glu Pro Val Trp
```

(handwritten annotations, right side): Some Error see p. 1

(handwritten annotation at line 493): Number of amino acids differ:
- 200 listed
- 210 shown (see next page)

```
        RAW SEQUENCE LISTING                    DATE: 05/31/2001
        PATENT APPLICATION:  US/09/785,738      TIME: 10:36:54

        Input Set : A:\es.txt
        Output Set: C:\CRF3\05312001\I785738.raw
```

```
       519                  165              170              175
       520 Thr Pro Tyr Asn Arg Pro Asn Asp His Leu Pro Ala Arg Gln Gln Tyr
       521              180              185              190
       522 Val Lys Asp Phe Val Glu Lys Asp Val Ser Ser His Ala Val Asp Ala
       523          195              200              205
       524 Thr Ala
E-->   525  ( 210 )        ===>   200 listed
       528 <210> SEQ ID NO: 11
       529 <211> LENGTH: 933
       530 <212> TYPE: DNA
       531 <213> ORGANISM: Cotton
       533 <220> FEATURE:
       534 <221> NAME/KEY: CDS
       535 <222> LOCATION: (33)..(635)
       537 <400> SEQUENCE: 11
       538 attttttttt aatttgacgg aaaaaaaaaa ct atg acc atg ggt tct gca gac   53
       539                                    Met Thr Met Gly Ser Ala Asp
W-->   540                                 1              5
W-->   542 aag agg gag gaa gtt att cag gca tgg tac atg gat gat agt gat gaa  101 Lys Arg
W-->   543 Glu Glu Val Ile Gln Ala Trp Tyr Met Asp Asp Ser Asp Glu
       544          10              15              20
W-->   546 gat cag agg ctt cct cat cac cgt gaa cct aag gaa tat gta tcc ttg  149 Asp Gln
W-->   547 Arg Leu Pro His His Arg Glu Pro Lys Glu Tyr Val Ser Leu
W-->   548      25              30              35
W-->   550 gat aaa ctt gct gag ctt gga gta ctc agc tgg cga ttg gat gct gat  197 Asp Lys
W-->   551 Leu Ala Glu Leu Gly Val Leu Ser Trp Arg Leu Asp Ala Asp
W-->   552  40              45              50              55
W-->   554 aac tat gaa aat gat gaa gag ttg aag aaa att cgt gaa gaa cga ggt  245 Asn Tyr
W-->   555 Glu Asn Asp Glu Glu Leu Lys Lys Ile Arg Glu Glu Arg Gly
W-->   556              60              65              70
W-->   558 tac tcc tac atg gac ttc tgc gag gtt tgc cct gag aag ctt cca aat  293 Tyr Ser
W-->   559 Tyr Met Asp Phe Cys Glu Val Cys Pro Glu Lys Leu Pro Asn
W-->   560              75              80              85
W-->   562 tat gag gag aag ata aaa aat ttc ttc gaa gaa cat att cat act gat  341 Tyr Glu
W-->   563 Glu Lys Ile Lys Asn Phe Phe Glu Glu His Ile His Thr Asp
W-->   564          90              95              100
W-->   566 gag gag atc cgt tac tgt gtg gca gga agt ggt tat ttt gat gta cgg  389 Glu Glu
W-->   567 Ile Arg Tyr Cys Val Ala Gly Ser Gly Tyr Phe Asp Val Arg
W-->   568      105              110              115
W-->   570 gat cat aat gat aaa tgg att cgt gtg tgg gtg aag aaa gga ggc atg  437 Asp His
W-->   571 Asn Asp Lys Trp Ile Arg Val Trp Val Lys Lys Gly Gly Met
W-->   572 120              125              130              135
W-->   574 ata gtt tta cct gct gga att tat cat cgc ttt act ctg gat aca gac  485 Ile Val
W-->   575 Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu Asp Thr Asp
W-->   576              140              145              150
W-->   578 aac tat att aag gca atg cgg ctc ttt gtt ggt gat cca att tgg act  533 Asn Tyr
W-->   579 Ile Lys Ala Met Arg Leu Phe Val Gly Asp Pro Ile Trp Thr
  -->   580              155              160              165
  -->   582 ccg tac aat cgt ccg cac gat cat ctt cct gca agg aag gag tat atc  581 Pro Tyr
```

```
W--> 583 Asn Arg Pro His Asp His Leu Pro Ala Arg Lys Glu Tyr Ile
W--> 584          170               175                 180
W--> 586 aag aac ttt ttg cgg gag gaa ggt ggt ggc caa gcc gtt gat gct gcc   629 Lys Asn
W--> 587 Phe Leu Arg Glu Glu Gly Gly Gly Gln Ala Val Asp Ala Ala
W--> 588          185               190                 195
W--> 590 gca taa aatcaacatt catctggtgg tggccaagtc gttgatgctg ccgcataaaa   685 Ala
W--> 591 200
E--> 593 tcagcattca tctctggtat cgtgtcttat aaaatatgaa accccggatt tgtggtaata 745
E--> 594 aataagtcta ggcttgtctg cttttgatgc gtggatatgg atcgttatgg ttgttgcttg 805
E--> 595 ctatatattg cctattccat atcgaaaatt cgcaaacttg ctatgtattt ctacatttta 865
E--> 596 tgtgcttact accagattgg ctcttaataa tcaaagttta cataatatac atttcgtcga 925
E--> 597 cgcggccg                                                          933
     633 <210> SEQ ID NO: 13
     634 <211> LENGTH: 919
     635 <212> TYPE: DNA
     636 <213> ORGANISM: Human
     638 <220> FEATURE:
     639 <221> NAME/KEY: CDS
     640 <222> LOCATION: (1)..(564)
     642 <400> SEQUENCE: 13
W--> 643 cga aca cgg cac ccg cac tgc gcg tca gtg gtg cag gcc tgg tat atg   48 Arg Thr Arg
W--> 644 His Pro His Cys Ala Ser Val Val Gln Ala Trp Tyr Met
W--> 645  1            5                   10                  15
W--> 647 gac gac gcc ccg ggc acc cgc ggc aac ccc acc gcc ccg acc ccg gcc   96 Asp Asp Ala
W--> 648 Pro Gly Thr Arg Gly Asn Pro Thr Ala Pro Thr Pro Ala
W--> 649             20              25                  30
W--> 651 gcc cag tgc gct gga gca gct gcg cgg ctc ggg gtg ctc tac tgg aag   144 Ala Gln
W--> 652 Cys Ala Gly Ala Ala Ala Arg Leu Gly Val Leu Tyr Trp Lys
W--> 653          35              40                  45
W--> 655 ctg gat gct gac aaa tat gag aat gat cca gaa tta gaa aag atc cga   192 Leu Asp
W--> 656 Ala Asp Lys Tyr Glu Asn Asp Pro Glu Leu Glu Lys Ile Arg
W--> 657          50              55                  60
W--> 659 aga gag agg aac tac tcc tgg atg gac atc ata acc ata tgc aaa gat   240 Arg Glu
W--> 660 Arg Asn Tyr Ser Trp Met Asp Ile Ile Thr Ile Cys Lys Asp
W--> 661 65                   70                  75                  80
W--> 663 aaa cta cca aat tat gaa gaa aag att aag atg ttc tac gag gag cat   288 Lys Leu
W--> 664 Pro Asn Tyr Glu Glu Lys Ile Lys Met Phe Tyr Glu Glu His
N--> 665                   85                  90                  95
N--> 667 ttg cac ttg gac gat gag atc cgc tac atc ctg gat ggc agt ggg tac   336 Leu His
N--> 668 Leu Asp Asp Glu Ile Arg Tyr Ile Leu Asp Gly Ser Gly Tyr
N--> 669              100             105                 110
N--> 671 ttc gat gtg agg gac aag gag gac cag tgg atc cgg atc ttc atg gag   384 Phe Asp
N--> 672 Val Arg Asp Lys Glu Asp Gln Trp Ile Arg Ile Phe Met Glu
N--> 673          115             120                 125
N--> 675 aag gga gac atg gtg acg ctc ccc gcg ggg atc tat cac cgc ttc acg   432 Lys Gly
N--> 676 Asp Met Val Thr Leu Pro Ala Gly Ile Tyr His Arg Phe Thr
N--> 677          130             135                 140
N--> 679 gtg gac gag aag aac tac acg aag gcc atg cgg ctg ttt gtg gga gaa   480 Val Asp
N--> 680 Glu Lys Asn Tyr Thr Lys Ala Met Arg Leu Phe Val Gly Glu
```

```
                    RAW SEQUENCE LISTING              DATE: 05/31/2001
                    PATENT APPLICATION:  US/09/785,738  TIME: 10:36:54

                    Input Set : A:\es.txt
                    Output Set: C:\CRF3\05312001\I785738.raw

W--> 681 145                     150                 155                 160
W--> 683 ccg gtg tgg aca gcg tac aac cgg ccc gct gac cat ttt gaa gcc cgc   528 Pro Val
W--> 684 Trp Thr Ala Tyr Asn Arg Pro Ala Asp His Phe Glu Ala Arg
W--> 685                          165                 170                 175
W--> 687 ggg cag tac gtg aaa ttt ctg gca cag acc gcc tag cagtgctgcc        574 Gly Gln
W--> 688 Tyr Val Lys Phe Leu Ala Gln Thr Ala
W--> 689                          180                 185
E--> 691 tgggaactaa cacgtgcctc gtaaaggtcc ccaatgtaat gaactgagca gaaaattcaa 634
E--> 692 tcaactttct ctttgctttt agaggatagc cttgaggtag attatctttc ctttgtaaga 694
E--> 693 ttatttgatc agaatatttt gtaatgaaag gatctagaaa gcaacttgga agtgtaaaga 754
E--> 694 gtcaccttca ttttctgtaa ctcaatcaag actggtgggt ccatggccct gtgttagttc 814
E--> 695 attgcattca ggttgagtcc caaatgaaag tttcatctcc cgaaatgcag ttccttagat 874
E--> 696 gcccatctgg acgtgaatgc cgcgcctgcg tgtaagaagg tgcaat                 920
     732 <210> SEQ ID NO: 15
     733 <211> LENGTH: 972
     734 <212> TYPE: DNA
     735 <213> ORGANISM: Mouse
     737 <220> FEATURE:
     738 <221> NAME/KEY: CDS
     739 <222> LOCATION: (17)..(556)
     741 <400> SEQUENCE: 15
     742 agccgccgcc gccacc atg gtg cag gcc tgg tat atg gac gag tcc acc gcc 52
     743                 Met Val Gln Ala Trp Tyr Met Asp Glu Ser Thr Ala
W--> 744                 1               5                   10
W--> 746 gac ccg cgg aag ccc cac cgc gca cag ccc gac cgc ccc gtg agc ctg   100 Asp Pro
W--> 747 Arg Lys Pro His Arg Ala Gln Pro Asp Arg Pro Val Ser Leu
     748           15                  20                  25
N--> 750 gag cag ctg cgc acg ctc gga gtg ctc tat tgg aag cta gat gct gac   148 Glu Gln
N--> 751 Leu Arg Thr Leu Gly Val Leu Tyr Trp Lys Leu Asp Ala Asp
N--> 752      30                  35                  40
N--> 754 aag tat gag aac gat cca gaa cta gaa aag atc cgg aaa atg aga aac   196 Lys Tyr
N--> 755 Glu Asn Asp Pro Glu Leu Glu Lys Ile Arg Lys Met Arg Asn
N--> 756 45                  50                  55                  60
N--> 758 tac tcc tgg atg gac atc atc acc ata tgc aaa gat aca ctt ccc aat   244 Tyr Ser
N--> 759 Trp Met Asp Ile Ile Thr Ile Cys Lys Asp Thr Leu Pro Asn
N--> 760                  65                  70                  75
N--> 762 tac gag gag aag atc aag atg ttc ttt gag gaa cat ctg cat ctg gat   292 Tyr Glu
N--> 763 Glu Lys Ile Lys Met Phe Phe Glu Glu His Leu His Leu Asp
N--> 764           80                  85                  90
N--> 766 gag gag atc cgc tac atc ctg gag ggt agt ggg tac ttc gat gtc agg   340 Glu Glu
N--> 767 Ile Arg Tyr Ile Leu Glu Gly Ser Gly Tyr Phe Asp Val Arg
N--> 768           95                  100                 105
N--> 770 gac aag gag gac aag tgg atc cgg att tcc atg gag aag ggg gac atg   388 Asp Lys
 --> 771 Glu Asp Lys Trp Ile Arg Ile Ser Met Glu Lys Gly Asp Met
 --> 772           110                 115                 120
 --> 774 att act ctt cct gcc ggc atc tat cac cgc ttc aca ctg gac gag aag   436 Ile Thr
 --> 775 Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu Asp Glu Lys
 --> 776           125                 130                 135                 140
 --> 778 aat tac gtg aag gcc atg cgg ctg ttt gtt gga gaa cct gtg tgg aca   484 Asn Tyr
```

```
RAW SEQUENCE LISTING              DATE: 05/31/2001
PATENT APPLICATION: US/09/785,738 TIME: 10:36:54

Input Set : A:\es.txt
Output Set: C:\CRF3\05312001\I785738.raw
```

```
W--> 779 Val Lys Ala Met Arg Leu Phe Val Gly Glu Pro Val Trp Thr
W--> 780               145                150                155
W--> 782 cca tac aac cgg cca gct gac cat ttt gat gcc cgt gta cag tac atg   532 Pro Tyr
W--> 783 Asn Arg Pro Ala Asp His Phe Asp Ala Arg Val Gln Tyr Met
W--> 784               160                165                170
W--> 786 agt ttt ttg gaa gga aca gca tag cagtgctcct caaagagaaa actgcactgt   586 Ser Phe
W--> 787 Leu Glu Gly Thr Ala
W--> 788               175                180
E--> 790 gtgaatctcc tgctgtggta accgaatgga aagttgctca cttttctgct tttgtatttg 646
E--> 791 aacttgaggc tagactagct ctctttgcta ggattgtgag atcagtgtct tttaaatgaa 706
E--> 792 agcctctcta aaagtgagtt ttacatggaa gccacaaaaa tgtgaaaaag tgaccttaat 766
E--> 793 tttccctaac tgtcaagact tagaggtata ggagccctgg attggtatgt gcattcatgc 826
E--> 794 atggccaatc ttcatctccc agatctttag gtgtctgttg gtgtgaagct atgcctcctg 886
E--> 795 caagagggca gttataacca gcacaactaa ccagatgacg tttttctcct ttgctgattg 946
E--> 796 ttgagtgggg aagtgggggtt gttgtt                                    972
    799 <210> SEQ ID NO: 16
    800 <211> LENGTH: 179
    801 <212> TYPE: PRT
    802 <213> ORGANISM: Mouse
    804 <400> SEQUENCE: 16
    805 Ala Ala Ala Ala Thr Met Val Gln Ala Trp Tyr Met Asp Glu Ser Thr
    806   1               5                10                15
    807 Ala Asp Pro Arg Lys Pro His Arg Ala Gln Pro Asp Arg Pro Val Ser
    808              20                25                30
    809 Leu Glu Gln Leu Arg Thr Leu Gly Val Leu Tyr Trp Lys Leu Asp Ala
    810             35                40                45
    811 Asp Lys Tyr Glu Asn Asp Pro Glu Leu Glu Lys Ile Arg Lys Met Arg
    812      50                55                60
    813 Asn Tyr Ser Trp Met Asp Ile Ile Thr Ile Cys Lys Asp Thr Leu Pro
    814 65                70                75                80
    815 Asn Tyr Glu Glu Lys Ile Lys Met Phe Phe Glu Glu His Leu His Leu
    816             85                90                95
    817 Asp Glu Glu Ile Arg Tyr Ile Leu Glu Gly Ser Gly Tyr Phe Asp Val
    818             100               105               110
    819 Arg Asp Lys Glu Asp Lys Trp Ile Arg Ile Ser Met Glu Lys Gly Asp
    820          115               120               125
    821 Met Ile Thr Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu Asp Glu
    822      130               135               140
    823 Lys Asn Tyr Val Lys Ala Met Arg Leu Phe Val Gly Glu Pro Val Trp
    824 145               150               155               160
    825 Thr Pro Tyr Asn Arg Pro Ala Asp His Phe Asp Ala Arg Val Gln Tyr
    826               165               170               175
    827 Met Ser Phe Leu Glu Gly Thr Ala
    828 180
    831 <210> SEQ ID NO: 17
    832 <211> LENGTH: 706
    833 <212> TYPE: DNA
    834 <213> ORGANISM: Zebrafish
    836 <220> FEATURE:
```

(handwritten annotations:)
Same
See p.1
Number of aminos differ:
- 179 listed
- 184 shown
180 (near line 828)

```
lo: //C \ C. [?] O
```

RAW SEQUENCE LISTING   DATE: 05/31/2001
PATENT APPLICATION: US/09/785,738   TIME: 10:36:54

Input Set : **A:\es.txt**
Output Set: **C:\CRF3\05312001\I785738.raw**

```
 837 <221> NAME/KEY: CDS                     Missing mandatory <220> to <223>
 838 <222> LOCATION: (36)..(581)  ←         features to explain the "n's" in
 840 <400> SEQUENCE: 17                      the sequence
 841 gtactgcgca tggagaccga accggactgt tcaag atg agt gtt ttc gag gca    53    See #9 on the
 842                                          Met Ser Val Phe Glu Ala            Error
W--> 843                                              1            5          Summary
W--> 845 tgg tac atg gat gaa gag tcc gga gag gac cag aga ctc ccg cac aaa  101 Trp Tyr   Sheet.
W--> 846 Met Asp Glu Glu Ser Gly Glu Asp Gln Arg Leu Pro His Lys
 847          10              15              20
W--> 849 ctg agc ccg aat cag ccc gtc agc gtc cag cag ctg gag cac atc gga  149 Leu Ser
W--> 850 Pro Asn Gln Pro Val Ser Val Gln Gln Leu Glu His Ile Gly
W--> 851          25              30              35
W--> 853 gtc ttt cac tgg aag ctg aac gct gat atc tat gaa aat gac ccc gaa  197 Val Phe
W--> 854 His Trp Lys Leu Asn Ala Asp Ile Tyr Glu Asn Asp Pro Glu
W--> 855          40              45              50
W--> 857 ctg cag aag atc cga gag gag aag ggt tat tcc ttt atg gac atc ata  245 Leu Gln    Same
W--> 858 Lys Ile Arg Glu Glu Lys Gly Tyr Ser Phe Met Asp Ile Ile                        error.
W--> 859 55              60              65              70                              see p.1
W--> 861 acc att cac ccg gac aaa ctg ccc gat tac caa aac aaa ctg aaa atg  293 Thr Ile
W--> 862 His Pro Asp Lys Leu Pro Asp Tyr Gln Asn Lys Leu Lys Met
W--> 863          75              80              85
W--> 865 ttt tac gaa gag cat ctc cac ctg gac gat gag atc cgt tat att ctg  341 Phe Tyr
W--> 866 Glu Glu His Leu His Leu Asp Asp Glu Ile Arg Tyr Ile Leu
W--> 867          90              95              100
W--> 869 gaa gga tcc tct tat ttt gat gtg cgg gac gaa ggc gac cgc tgg atc  389 Glu Gly
N--> 870 Ser Ser Tyr Phe Asp Val Arg Asp Glu Gly Asp Arg Trp Ile
N--> 871          105             110             115
N--> 873 cga ata gcg gtg tct aaa ggc gac ctc atc act tta ccg gcc ggg att  437 Arg Ile
N--> 874 Ala Val Ser Lys Gly Asp Leu Ile Thr Leu Pro Ala Gly Ile
N--> 875          120             125             130
N--> 877 tac cac aga ttc acc gtg gac gaa agc aac tac act aaa gcc atg cgt  485 Tyr His
N--> 878 Arg Phe Thr Val Asp Glu Ser Asn Tyr Thr Lys Ala Met Arg
N--> 879 135             140             145             150
N--> 881 ctg ttc gtg ggt gaa ccc gtc tgg aag gcc tac aac cgt cca gcc gat  533 Leu Phe
N--> 882 Val Gly Glu Pro Val Trp Lys Ala Tyr Asn Arg Pro Ala Asp
N--> 883          155             160             165
 --> 885 gac ttt gac atc cgc aag gaa tac gtg aac tcg ctg gga agc tcc tga  581 Asp Phe
 --> 886 Asp Ile Arg Lys Glu Tyr Val Asn Ser Leu Gly Ser Ser
 --> 887          170             175             180
 --> 889 aatgcctgat gggattgatt tagtgctgag aatcagactc tgcggtgcct tanacagaca 641
 --> 890 nncagcaata gtagagctaa catgtcatta cttagtcatc aagacacacc tgatataaag 701
 --> 891 attat                                               706
```

e://C:\Crf3\Outhold\I785738

VERIFICATION SUMMARY　　　　　　　　DATE: 05/31/2001
PATENT APPLICATION: **US/09/785,738**　　TIME: 10:36:55

Input Set : **A:\es.txt**
Output Set: **C:\CRF3\05312001\I785738.raw**

```
L:11 M:270 C: Current Application Number differs, Replaced Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:31 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:33 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:34 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:35 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:37 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:38 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:39 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:41 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:42 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:43 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:45 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:46 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:47 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:49 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:50 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:51 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:53 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:54 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:55 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:57 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:58 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:59 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:61 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:62 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:63 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:65 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:66 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:67 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:69 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:70 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:71 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:73 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:74 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:75 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:77 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:13
L:78 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:79 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
⌐:81 M:254 E: No. of Bases conflict, LENGTH:Input:748 Counted:170 SEQ:1
⌐:82 M:254 E: No. of Bases conflict, LENGTH:Input:808 Counted:230 SEQ:1
⌐:83 M:254 E: No. of Bases conflict, LENGTH:Input:868 Counted:290 SEQ:1
⌐:84 M:254 E: No. of Bases conflict, LENGTH:Input:872 Counted:294 SEQ:1
⌐:84 M:252 E: No. of Seq. differs, <211>LENGTH:Input:872 Found:294 SEQ:1
⌐:135 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
⌐:137 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
⌐:138 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
⌐:141 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
```

VERIFICATION SUMMARY   DATE: 05/31/2001
PATENT APPLICATION: US/09/785,738   TIME: 10:36:55

Input Set : **A:\es.txt**
Output Set: **C:\CRF3\05312001\I785738.raw**

```
L:142 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:143 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:145 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:146 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:147 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:149 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:150 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:151 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:153 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:154 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:155 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:157 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:158 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:159 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:161 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:162 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:163 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:165 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:166 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:167 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:169 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:170 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:171 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:173 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:174 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:175 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:177 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:178 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:179 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:181 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:14
L:182 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:183 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:185 M:254 E: No. of Bases conflict, LENGTH:Input:805 Counted:231 SEQ:3
L:186 M:254 E: No. of Bases conflict, LENGTH:Input:865 Counted:291 SEQ:3
L:187 M:254 E: No. of Bases conflict, LENGTH:Input:925 Counted:351 SEQ:3
L:188 M:254 E: No. of Bases conflict, LENGTH:Input:980 Counted:406 SEQ:3
L:188 M:252 E: No. of Seq. differs, <211>LENGTH:Input:980 Found:406 SEQ:3
L:235 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:236 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:237 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:239 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:240 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:241 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:243 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:244 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:245 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:247 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:248 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:249 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
```

VERIFICATION SUMMARY   DATE: 05/31/2001
PATENT APPLICATION: **US/09/785,738**   TIME: 10:36:55

Input Set : **A:\es.txt**
Output Set: **C:\CRF3\05312001\I785738.raw**

```
L:251 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:252 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:253 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:255 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:256 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:257 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:259 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:260 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:261 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:263 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:264 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:265 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:267 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:268 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:269 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:271 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:272 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:273 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:275 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:276 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:277 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:279 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:280 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:281 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:283 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:10
L:284 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:285 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:287 M:254 E: No. of Bases conflict, LENGTH:Input:691 Counted:60 SEQ:5
L:288 M:254 E: No. of Bases conflict, LENGTH:Input:751 Counted:120 SEQ:5
L:289 M:254 E: No. of Bases conflict, LENGTH:Input:774 Counted:143 SEQ:5
L:289 M:252 E: No. of Seq. differs, <211>LENGTH:Input:774 Found:143 SEQ:5
L:337 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:338 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:339 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:341 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:342 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:343 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:345 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:346 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:347 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:349 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:350 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:351 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:353 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:354 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:355 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:357 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:358 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:359 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
```

VERIFICATION SUMMARY   DATE: 05/31/2001
PATENT APPLICATION: **US/09/785,738**   TIME: 10:36:55

Input Set : **A:\es.txt**
Output Set: **C:\CRF3\05312001\I785738.raw**

```
L:361 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:362 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:363 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:365 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:366 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:367 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:369 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:370 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:371 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:372 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:373 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:374 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:376 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:377 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:378 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:380 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:16
L:381 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:382 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:384 M:254 E: No. of Bases conflict, LENGTH:Input:603 Counted:31 SEQ:7
L:384 M:252 E: No. of Seq. differs, <211>LENGTH:Input:603 Found:31 SEQ:7
L:432 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:434 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:434 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:435 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:435 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:438 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:438 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:439 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:439 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:440 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:442 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:442 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:443 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:443 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:444 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:446 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:446 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:447 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:447 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:448 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:450 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:450 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:451 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:451 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:452 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:454 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:454 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:455 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:455 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
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VERIFICATION SUMMARY   DATE: 05/31/2001
PATENT APPLICATION: US/09/785,738   TIME: 10:36:55

Input Set : A:\es.txt
Output Set: C:\CRF3\05312001\I785738.raw

L:456 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:458 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:458 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:459 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:459 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:460 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:462 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:462 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:463 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:463 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:464 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:466 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:466 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:467 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:467 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:468 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:470 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:470 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:471 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:471 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:472 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:474 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:474 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:475 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:475 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:476 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:478 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:478 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:479 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:479 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:480 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:482 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:8
L:482 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:483 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:485 M:254 E: No. of Bases conflict, LENGTH:Input:744 Counted:112 SEQ:9
L:486 M:254 E: No. of Bases conflict, LENGTH:Input:804 Counted:172 SEQ:9
L:487 M:254 E: No. of Bases conflict, LENGTH:Input:864 Counted:232 SEQ:9
L:488 M:254 E: No. of Bases conflict, LENGTH:Input:889 Counted:257 SEQ:9
L:488 M:252 E: No. of Seq. differs, <211>LENGTH:Input:889 Found:257 SEQ:9
L:525 M:252 E: No. of Seq. differs, <211>LENGTH:Input:200 Found:210 SEQ:10
L:540 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:542 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:542 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:543 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:543 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:546 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:546 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:547 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:547 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11

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VERIFICATION SUMMARY   DATE: 05/31/2001
PATENT APPLICATION: **US/09/785,738**   TIME: 10:36:55

Input Set : **A:\es.txt**
Output Set: **C:\CRF3\05312001\I785738.raw**

```
L:548 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:550 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:550 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:551 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:551 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:552 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:554 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:554 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:555 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:555 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:556 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:558 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:558 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:559 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:559 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:560 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:562 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:562 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:563 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:563 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:564 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:566 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:566 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:567 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:567 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:568 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:570 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:570 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:571 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:571 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:572 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:574 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:574 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:575 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:575 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:576 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:578 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:578 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:579 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:579 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:580 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:582 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:582 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:583 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:583 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:584 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:586 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:586 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:587 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
```

```
L:587 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:588 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:590 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:8
L:590 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:591 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:593 M:254 E: No. of Bases conflict, LENGTH:Input:745 Counted:113 SEQ:11
L:594 M:254 E: No. of Bases conflict, LENGTH:Input:805 Counted:173 SEQ:11
L:595 M:254 E: No. of Bases conflict, LENGTH:Input:865 Counted:233 SEQ:11
L:596 M:254 E: No. of Bases conflict, LENGTH:Input:925 Counted:293 SEQ:11
L:597 M:254 E: No. of Bases conflict, LENGTH:Input:933 Counted:301 SEQ:11
L:597 M:252 E: No. of Seq. differs, <211>LENGTH:Input:933 Found:301 SEQ:11
L:643 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:644 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:645 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:647 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:648 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:649 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:651 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:652 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:653 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:655 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:656 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:657 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:659 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:660 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:661 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:663 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:664 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:665 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:667 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:668 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:669 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:671 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:672 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:673 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:675 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:676 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:677 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:679 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:680 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:681 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:683 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:684 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:685 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:687 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:14
L:688 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:689 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:691 M:254 E: No. of Bases conflict, LENGTH:Input:634 Counted:60 SEQ:13
L:692 M:254 E: No. of Bases conflict, LENGTH:Input:694 Counted:120 SEQ:13
```

VERIFICATION SUMMARY   DATE: 05/31/2001
PATENT APPLICATION: **US/09/785,738**   TIME: 10:36:55

Input Set : **A:\es.txt**
Output Set: **C:\CRF3\05312001\I785738.raw**

```
L:693 M:254 E: No. of Bases conflict, LENGTH:Input:754 Counted:180 SEQ:13
L:694 M:254 E: No. of Bases conflict, LENGTH:Input:814 Counted:240 SEQ:13
L:695 M:254 E: No. of Bases conflict, LENGTH:Input:874 Counted:300 SEQ:13
L:696 M:254 E: No. of Bases conflict, LENGTH:Input:920 Counted:346 SEQ:13
L:696 M:252 E: No. of Seq. differs, <211>LENGTH:Input:919 Found:346 SEQ:13
L:744 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:746 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:747 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:750 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:751 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:752 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:754 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:755 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:756 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:758 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:759 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:760 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:762 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:763 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:764 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:766 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:767 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:768 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:770 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:771 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:772 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:774 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:775 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:776 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:778 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:779 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:780 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:782 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:783 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:784 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:786 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:12
L:787 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:788 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:790 M:254 E: No. of Bases conflict, LENGTH:Input:646 Counted:112 SEQ:15
L:791 M:254 E: No. of Bases conflict, LENGTH:Input:706 Counted:172 SEQ:15
L:792 M:254 E: No. of Bases conflict, LENGTH:Input:766 Counted:232 SEQ:15
L:793 M:254 E: No. of Bases conflict, LENGTH:Input:826 Counted:292 SEQ:15
L:794 M:254 E: No. of Bases conflict, LENGTH:Input:886 Counted:352 SEQ:15
L:795 M:254 E: No. of Bases conflict, LENGTH:Input:946 Counted:412 SEQ:15
L:796 M:254 E: No. of Bases conflict, LENGTH:Input:972 Counted:438 SEQ:15
L:796 M:252 E: No. of Seq. differs, <211>LENGTH:Input:972 Found:438 SEQ:15
L:828 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:828 M:252 E: No. of Seq. differs, <211>LENGTH:Input:179 Found:184 SEQ:16
L:843 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
```

VERIFICATION SUMMARY   DATE: 05/31/2001
PATENT APPLICATION: **US/09/785,738**   TIME: 10:36:55

Input Set : **A:\es.txt**
Output Set: **C:\CRF3\05312001\I785738.raw**

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L:845 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:846 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:849 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:850 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:851 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:853 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:854 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:855 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:857 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:858 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:859 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:861 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:862 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:863 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:865 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:866 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:867 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:869 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:870 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:871 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:873 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:874 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:875 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:877 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:878 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:879 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:881 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:882 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:883 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:885 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:886 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:887 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:889 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:17
L:889 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:889 M:254 E: No. of Bases conflict, LENGTH:Input:641 Counted:113 SEQ:17
L:890 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:17
L:890 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:890 M:254 E: No. of Bases conflict, LENGTH:Input:701 Counted:173 SEQ:17
L:891 M:254 E: No. of Bases conflict, LENGTH:Input:706 Counted:178 SEQ:17
L:891 M:252 E: No. of Seq. differs, <211>LENGTH:Input:706 Found:178 SEQ:17
```